

A7 structure visualization; and computer functionality for protein sequence and structural analysis; and database searching tools.

A8 SUB C6 } 28
27. (Amended) The method of claim 1, further after generating the 3-D structural variant models, exporting some or all of the[m] models into a program that computationally docks the models with test compounds to assess intermolecular interactions.

A9 F28 49
48. (Amended) The method of claim 44, wherein the target is enzyme expressed by [a] an infectious agent.

A10 54
53. (Amended) A database, comprising:
sequences of nucleotides encoding a protein or portions thereof, wherein proteins comprise polymorphic variants; and the portions encode a domain of the protein that comprises a site in the protein that binds to a drug candidate[s]; and the coordinates of 3-dimensional (3-D) structures of the encoded proteins or portions thereof.

A11 57 56
56. (Amended) The database of claim 53 that comprises [at] more than 10, more than 100, more than 1000, more than 8000, or more than 10,000 polymorphic variants and the corresponding 3-D structures.

REMARKS

Any fees that may be due in connection with filing this paper, or during the entire pendency of this application, may be charged to Deposit Account No. 50-1213.

The amendments to the specification and to claims 7, 8, 21, 27, 48, and 56 correct obvious typographical errors, correct citations of publications, and produce

U.S.S.N. 09/709,905
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Preliminary Amendment

grammatical clarity. The amendment to claim 23 corrects a typographical error and finds basis in claim 12.

No new matter has been added.

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Entry of this amendment and examination of the application are respectfully requested.

Respectfully submitted,
HELLER, EHRMAN, WHITE & McAULIFFE LLP

By:


Stephanie L. Seidman
Registration No. 33,779

Attorney Docket No. 24737-1906C
Address all correspondence to:
Stephanie L. Seidman, Esq.
HELLER EHRMAN WHITE & McAULIFFE LLP
4250 Executive Square, 7th Floor
La Jolla, California 92037-9103
Telephone: (619) 450-8400
Facsimile: (619) 587-5360
EMAIL: sseidman@hewm.com